Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1-18. (Cancelled)

19. (Presently Amended) An antibody or an antigen binding fragment thereof ~~having~~ comprising ~~the~~ a complementarity determining region-H3 (CDR-H3) ~~CDR-H3~~ sequence selected from the group consisting of: SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 30, and SEQ ID NO: 31.

20. (Presently Amended) An antibody or an antigen binding fragment thereof ~~having~~ comprising ~~the~~ a complementarity determining region-L3 (CDR-L3) ~~CDR-H3~~ sequence selected from the group consisting of: SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34.

21. (Presently Amended) An antibody or an antigen binding fragment thereof ~~having~~ comprising a complementarity determining region-H3 (CDR-H3) ~~CDR-H3~~ sequence selected from the group consisting of: SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 30, and SEQ ID NO: 31 and a complementarity determining region-L3 (CDR-L3) ~~CDR-L3~~ sequence selected from the group consisting of: SEQ ID NO: 32, SEQ ID NO: 33 and SEQ ID NO: 34.

22. (Presently Amended) A method for identifying candidate antigen-specific sequences ~~of at least the CDR3 region~~ of antibodies specific against at least one antigen produced by *Clostridium difficile*, ~~during an infection or against a vaccine~~, the method comprising ~~the steps of~~:

(i) ~~with B cells isolated from at least one patient who has been infected by *Clostridium difficile* or administered said vaccine,~~ obtaining B cells from at least one patient whose immune system has been exposed to the antigen and sequencing from the B-cells at least ~~the~~ complementarity determining region-3 (CDR3) regions of ~~CDR3 region of the of the VH and/or VL~~ variable heavy chains (VH) or variable light chains (VL), or both ~~regions of said B cells~~; and

(ii) ~~correlating said sequences of at least the CDR3 regions of the VH and/or VL coding regions of said B cells from said at least one patient to identify~~ detecting a set of ~~candidate~~ sequences ~~for at least a CDR3 region~~ that occur in total at a frequency of at least one percent ~~of antibodies specific against said at least one antigen produced by *Clostridium difficile* or against said vaccine~~, wherein the ~~each of said~~ set of ~~candidate CDR3~~ sequences include a dominant sequence and sequences ~~or a sequence having~~ of at least 80% homology to the dominant sequence. ~~therewith occurring in total at a frequency of at least 1 percent in the set of sequences determined at step (i).~~

23. (Presently amended) [[A]] The method ~~according to~~ of claim 22, ~~said~~ wherein the B cells are ~~being selected from the group consisting of~~ peripheral B-cell lymphocytes or ~~and~~ B cells from the spleen.

24. (Presently amended) [[A]] The method ~~according to~~ of claim [[23]] 22, ~~said peripheral B-cell lymphocytes being~~ wherein the B cells are isolated from blood ~~from said at least one patient~~.

25. (Presently amended) [[A]] The method ~~according to~~ of claim 22, ~~said at least one~~ wherein the antigen ~~being~~ is an immunogen.

26. (Presently amended) [[A]] The method ~~according to~~ of claim 22, ~~said at least one~~ wherein the patient displays ~~displaying~~ a pronounced antibody response in response to infection by *Clostridium difficile*.

27. (Presently amended) [[A]] The method ~~according to~~ of claim 22, ~~said at least one patient having~~ wherein the patient has recovered from infection by *Clostridium difficile*.

28. (Presently amended) [[A]] The method ~~according to~~ of claim 22, ~~said correlation~~ wherein step (i) comprises sequencing DNA or RNA from the B cells and step (ii) comprises ~~comprising~~ determining putative amino acid sequences based on the DNA or RNA sequences ~~sequenced regions from said sequences of at least the VH and/or VL CDR3 coding regions,~~ and wherein the set of sequences is detected among the ~~correlating said~~ putative amino acid sequences.

29. (Presently amended) [[A]] The method ~~according to~~ of claim [[27]] 22, ~~said correlation~~ wherein step (ii) further comprises ~~comprising~~ identifying CDR2 regions and detecting a set of candidate sequences among the CDR2 regions ~~the Complementarity Determining Regions in said at least the VH and/or VL regions andcorrelating said Complementarity Determining Regions~~.

30. (Presently amended) [[A]] The method ~~according to~~ of claim 29, wherein step (ii) further comprises identifying CDR1 regions and detecting a set of candidate sequences among the CDR1 regions ~~said Complementarity Determining Regions being selected from the group consisting of CDR1, CDR2 and CDR3~~.

31. (Presently amended) [[A]] The method ~~according to~~ of claim 22, ~~said correlation~~ wherein step (ii) ~~additionally correlating at least one of the group consisting of:~~ further comprises determining at least one factor from the group consisting of: the strain of *Clostridium difficile*

infecting the patient; ~~infecting said at least one patient~~, the time point at which ~~said~~ the B cells are isolated during infection; ~~of said at least one patient by *Clostridium difficile*~~, ~~and~~ the age of ~~said at least one~~ the patient;[,] the sex ~~of said at least one~~ the patient;[,] and the race of ~~said at least one~~ the patient;[,] and correlating the factor with the candidate sequence.

32. (Presently amended) [[A]] The method ~~according to~~ of claim 22, wherein the ~~said~~ B cells ~~having been~~ are isolated from the ~~said at least one~~ patient at a plurality of time points during infection ~~of said at least one patient by *Clostridium difficile*, said correlation step (ii) correlating the time point during infection of said at least one patient by *Clostridium difficile* at which said B cells are isolated~~.

33. (Presently amended) [[A]] The method of claim 22, ~~said~~ wherein the B cells ~~having been~~ are isolated from at least two patients, ~~at least~~ one of whom has recovered from infection by ~~from~~ *Clostridium difficile*, and ~~at least~~ one of whom has not recovered from infection by *Clostridium difficile*, and wherein sequences from the recovered patient are compared with sequences from the patient who has not recovered to identify sequences that are not effective to clear the infection ~~said correlation step (ii) correlating the recovery of said at least two patients from infection by *Clostridium difficile*~~.

34. (Presently amended) [[A]] The method ~~according to~~ of claim 22, ~~said~~ wherein the B cells ~~having been~~ are isolated from at least two patients, ~~said~~ wherein each patient ~~patients being~~ has been infected by a strain ~~different strains~~ of *Clostridium difficile* different from the strain that has infected the other ~~producing said at least one antigen, said correlation~~ and wherein sequences from one patient are compared with sequences from the other patient ~~step (ii) further correlating said sequence of at least the VH and/or or VL coding regions of said B cells~~ to identify a set of candidate sequences for antibodies, each of which is specific against at least one shared antigen produced by ~~said~~ the different strains of *Clostridium difficile* ~~or is specific against different antigens produced by said different strains of *Clostridium difficile*~~.

35. (Presently amended) A method of producing a database which identifies candidate sequences for antibodies specific against at least one antigen produced ~~produces~~ by *Clostridium difficile*, comprising the steps of:

(i) performing [[a]] the method according to claim 22; and

(ii) storing the data produced by said method in the ~~said~~ database.

36. (Presently amended) A method of generating a report which identifies candidate sequences for antibodies specific against at least one antigen produced by *Clostridium difficile*, comprising the steps of:

(i) performing [[a]] the method according to claim 22; and

(ii) producing a report comprising the data produced by the ~~said~~ method.

37. (New) A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 19.

38. (New) A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 20.

39. (New) A method for treating an infection by *Clostridium difficile* in a patient, the method comprising administering to the patient a pharmaceutically effective amount of the antibody or the antigen binding fragment thereof of claim 21.